

In the Claims:

Please cancel Claims 19-20 without prejudice to or disclaimer of the subject matter therein.

Please amend Claim 1 as follows.

1. (Once Amended) A method for determining the haplotype structure of a contiguous DNA segment comprising a first nucleotide polymorphism (NP) and a second NP separated by at least 200 nucleotides, said method comprising:
 - (a) obtaining a DNA sample comprising said contiguous DNA segment;
 - (b) using said DNA sample as a template for polymerase chain reaction (PCR) amplification of a DNA fragment comprising said contiguous DNA segment, wherein the PCR amplification is performed with
 - a first primer capable of annealing to a region adjacent to the first NP and distal to the second NP and
 - a second primer capable of annealing to a region adjacent to the second NP and distal to the first NP;
 - (c) ligating the ends of said DNA fragment to each other so as to produce a circular DNA molecule; and
 - (d) determining the haplotype of said first NP and said second NP.

Please add the following new Claims 21 and 22:

21. (New) A method for determining the haplotype structure of a contiguous DNA segment comprising a first nucleotide polymorphism (NP) and a second NP separated by at least 200 nucleotides, said method comprising:
 - (a) obtaining a DNA sample comprising said contiguous DNA segment, wherein the DNA segment further comprises
 - a DNA sequence immediately 5' to the first NP that encompasses an annealing site for a primer and

a DNA sequence immediately 3' to the second NP that encompasses an annealing site for a primer;

(b) using said DNA sample as a template for polymerase chain reaction (PCR) amplification utilizing said primers of a DNA fragment comprising said contiguous DNA segment;

(c) ligating the ends of said DNA fragment to each other so as to produce a circular DNA molecule; and

(d) determining the haplotype of said first NP and said second NP.

22. (New) The method of 21, wherein the DNA sequence immediately 5' to the first NP has a length selected from the group consisting of:

less than 500, less than 400, less than 300, less than 200, less than 100, and less than 50 bases long; and,

wherein the DNA sequence immediately 3' to the second NP has a length selected from the group consisting of:

less than 500, less than 400, less than 300, less than 200, less than 100, and less than 50 bases long.